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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/903,325A

DATE: 03/13/2002

TIME: 11:17:12

Input Set : A:\510015-257.TXT

Output Set: N:\CRF3\03132002\I903325A.raw

4 <110> APPLICANT: De Robertis, Edward M.
 5 Bouwmeester, Tewis
 8 <120> TITLE OF INVENTION: Endoderm, Cardiac and Neural Inducing
 9 Factors
 11 <130> FILE REFERENCE: 510015-257
 13 <140> CURRENT APPLICATION NUMBER: US 09/903,325A
 C--> 14 <141> CURRENT FILING DATE: 2001-11-07
 16 <150> PRIOR APPLICATION NUMBER: US 60/020,150
 17 <151> PRIOR FILING DATE: 1996-06-20
 19 <160> NUMBER OF SEQ ID NOS: 10
 21 <170> SOFTWARE: FastSEQ for Windows Version 3.0
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 24 <211> LENGTH: 270
 25 <212> TYPE: PRT
 26 <213> ORGANISM: Xenopus
 28 <400> SEQUENCE: 1
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 31 Asp Gly Ala Gly Lys His Ser Glu Gly Arg Glu Arg Thr Lys Thr Tyr
 32 20 25 30
 33 Ser Leu Asn Ser Arg Gly Tyr Phe Arg Lys Glu Arg Gly Ala Arg Arg
 34 35 40 45
 35 Ser Lys Ile Leu Leu Val Asn Thr Lys Gly Leu Asp Glu Pro His Ile
 36 50 55 60
 37 Gly His Gly Asp Phe Gly Leu Val Ala Glu Leu Phe Asp Ser Thr Arg
 38 65 70 75 80
 39 Thr His Thr Asn Arg Lys Glu Pro Asp Met Asn Lys Val Lys Leu Phe
 40 85 90 95
 41 Ser Thr Val Ala His Gly Asn Lys Ser Ala Arg Arg Lys Ala Tyr Asn
 42 100 105 110
 43 Gly Ser Arg Arg Asn Ile Phe Ser Arg Arg Ser Phe Asp Lys Arg Asn
 44 115 120 125
 45 Thr Glu Val Thr Glu Lys Pro Gly Ala Lys Met Phe Trp Asn Asn Phe
 46 130 135 140
 47 Leu Val Lys Met Asn Gly Ala Pro Gln Asn Thr Ser His Gly Ser Lys
 48 145 150 155 160
 49 Ala Gln Glu Ile Met Lys Glu Ala Cys Lys Thr Leu Pro Phe Thr Gln
 50 165 170 175
 51 Asn Ile Val His Glu Asn Cys Asp Arg Met Val Ile Gln Asn Asn Leu
 52 180 185 190
 53 Cys Phe Gly Lys Cys Ile Ser Leu His Val Pro Asn Gln Gln Asp Arg
 54 195 200 205
 55 Arg Asn Thr Cys Ser His Cys Leu Pro Ser Lys Phe Thr Leu Asn His

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56      210      215      220
57 Leu Thr Leu Asn Cys Thr Gly Ser Lys Asn Val Val Lys Val Val Met
58 225      230      235      240
59 Met Val Glu Glu Cys Thr Cys Glu Ala His Lys Ser Asn Phe His Gln
60      245      250      255
61 Thr Ala Gln Phe Asn Met Asp Thr Ser Thr Thr Leu His His
62      260      265      270
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65 <211> LENGTH: 1338
66 <212> TYPE: DNA
67 <213> ORGANISM: Xenopus
69 <400> SEQUENCE: 2
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71 atgtactcag gatctgtatt atcgtctgcc ttgtgaatga tggagcagga aaacactcag      120
72 aaggacgaga aaggacaaaa acatattcac ttaacagcag aggttacttc agaaaagaaa      180
73 gaggagcacg taggagcaag attctgctgg tgaatactaa aggtcttgat gaaccccaca      240
74 ttgggcatgg tgattttcgc ttagtagctg aactatttga ttccaccaga acacatacaa      300
75 acagaaaaga gccagacatg aacaaagtca agcttttctc aacagttgcc catggaaaca      360
76 aaagtgcagg aagaaaaagct tacaatgggt ctagaaggaa tatttttctt cgccgttctt      420
77 ttgataaaag aaatacagag gttactgaaa agcctgggtgc caagatgttc tggaaacaatt      480
78 ttttggttaa aatgaatgga gcccacaga atacaagcca tggcagtaaa gcacaggaaa      540
79 taatgaaaga agcttgcaaa accttgtttt tcaactcagaa tattgtacat gaaaactgtg      600
80 acaggatggt gatacagaac aatctgtgct ttggtaaatg catctctctc catgttccaa      660
81 atcagcaaga tcgacgaaat acttgttccc attgcttgcc gtccaaattt accctgaacc      720
82 acctgacgct gaattgtact ggatctaaga atgtagtaaa ggttgtcatg atggtagagg      780
83 aatgcacgtg tgaagctcat aagagcaact tccaccaaac tgcacagttt aacatggata      840
84 catctactac cctgcaccat taaaggactg ccatacagta tggaaatgcc cttttgttgg      900
85 aatatttgtt acatactatg catctaaagc attatgttgc cttctatttc atataaccac      960
86 atggaataag gattgtatga attataatta acaaatggca ttttgtgtaa catgcaagat      1020
87 ctctgttcca tcagttgcaa gataaaaggc aatatttgtt tgactttttt tctacaaaat      1080
88 gaatacccaa atatatgata agataatggg gtcaaaactg ttaaggggta atgtaataat      1140
89 agggactaag tttgcccagg agcagtgacc cataacaacc aatcagcagg tatgatttac      1200
90 tggtcacctg tttaaaagca aacatcttat tggttgctat gggttactgc ttctgggcaa      1260
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94 <210> SEQ ID NO: 3
95 <211> LENGTH: 318
96 <212> TYPE: PRT
97 <213> ORGANISM: Xenopus frazzled
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102 Gly Leu Ala Leu Leu Leu Leu Pro Asn Ala Tyr Cys Ala Ser Cys Glu
103      20      25      30
104 Pro Val Arg Ile Pro Met Cys Lys Ser Met Pro Trp Asn Met Thr Lys
105      35      40      45
106 Met Pro Asn His Leu His His Ser Thr Gln Ala Asn Ala Ile Leu Ala
107      50      55      60
108 Ile Glu Gln Phe Glu Gly Leu Leu Thr Thr Glu Cys Ser Gln Asp Leu

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109 65
110 Leu Phe Phe Leu Cys Ala Met Tyr Ala Pro Ile Cys Thr Ile Asp Phe
111 85 90 95
112 Gln His Glu Pro Ile Lys Pro Cys Lys Ser Val Cys Glu Arg Ala Arg
113 100 105 110
114 Ala Gly Cys Glu Pro Ile Leu Ile Lys Tyr Arg His Thr Trp Pro Glu
115 115 120 125
116 Ser Leu Ala Cys Glu Glu Leu Pro Val Tyr Asp Arg Gly Val Cys Ile
117 130 135 140
118 Ser Pro Glu Ala Ile Val Thr Val Glu Gln Gly Thr Asp Ser Met Pro
119 145 150 155 160
120 Asp Phe Ser Met Asp Ser Asn Asn Gly Asn Cys Gly Ser Gly Arg Glu
121 165 170 175
122 His Cys Lys Cys Lys Pro Met Lys Ala Thr Gln Lys Thr Tyr Leu Lys
123 180 185 190
124 Asn Asn Tyr Asn Tyr Val Ile Arg Ala Lys Val Lys Glu Val Lys Val
125 195 200 205
126 Lys Cys His Asp Ala Thr Ala Ile Val Glu Val Lys Glu Ile Leu Lys
127 210 215 220
128 Ser Ser Leu Val Asn Ile Pro Lys Asp Thr Val Thr Leu Tyr Thr Asn
129 225 230 235 240
130 Ser Gly Cys Leu Cys Pro Gln Leu Val Ala Asn Glu Glu Tyr Ile Ile
131 245 250 255
132 Met Gly Tyr Glu Asp Lys Glu Arg Thr Arg Leu Leu Leu Val Glu Gly
133 260 265 270
134 Ser Leu Ala Glu Lys Trp Arg Asp Arg Leu Ala Lys Lys Val Lys Arg
135 275 280 285
136 Trp Asp Gln Lys Leu Arg Arg Pro Arg Lys Ser Lys Asp Pro Val Ala
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143 <212> TYPE: DNA
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149 ctaattctgc acttttaaatt tatctgagta attgttcatt ttgtattgga tgggactaaa 180
150 gataaactta actccttgct tttgacttgc ccataaacta taagggtggg tgagttgtag 240
151 ttgcttttac atgtgccag attttcctg tattccctgt attccctcta aagtaagcct 300
152 acacatacag gttgggcaga ataacaatgt ctgaacaag gaaagtggac tcattactgc 360
153 tactggccat acctggactg gcgtttctct tattacccaa tgcttactgt gcttcgtgtg 420
154 agcctgtgcg gatcccatg tgcaaatota tgccatggaa catgaccaag atgcccacc 480
155 atctccacca cagcactcaa gccaatgcca tcctggcaat tgaacagttt gaaggtttgc 540
156 tgaccactga atgtagccag gaccttttgt tctttctgtg tgccatgtat gccccattt 600
157 gtaccatcga tttccagcat gaaccaatta agcettgcaa gtccgtgtgc gaaaggcca 660
158 gggccggctg tgagccatt ctcataaagt accggcacac ttggccagag agcctggcat 720
159 gtgaagagct gccgtatat gacagaggag tctgcatctc cccagaggct atcgtcacag 780

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160  tggacaagc aacagattca atgccagact tctccatgga ttcaacaat ggaaattgcg      840
161  gaagcggcag ggagcactgt aaatgcaagc ccatgaaggc aacccaaaag acgtatctca      900
162  agaataatta caattatgta atcagagcaa aagtgaagaa ggtgaaagtg aaatgccacg      960
163  acgcaacagc aattgtggaa gtaaaggaga ttctcaagtc ttccctagtg aacattccta    1020
164  aagacacagt gacactgtac accaactcag gctgcttggt cccccagctt gttgccaatg    1080
165  aggaatacat aattatgggc tatgaagaca aagagcgtac caggcttcta ctagtggaag    1140
166  gatccttggc cgaaaaatgg agagatcgtc ttgctaagaa agtcaagcgc tgggatcaaa    1200
167  agcttcgacg tcccaggaaa agcaaagacc ccgtggctcc aattcccaac aaaaacagca    1260
168  attccagaca agcgcgtagt tagactaacg gaaaggtgta tggaaactct atggactttg    1320
169  aaactaagat ttgcattggt ggaagagcaa aaaagaaatt gcactacagc acgttatatt    1380
170  ctattgttta ctacaagaag ctggtttagt tgattgtagt tctcctttcc ttcttttttt    1440
171  ttataactat atttgcacgt gttcccaggc aattgtttta ttcaacttcc agtgacagag    1500
172  cagtgaactga atgtctcagc ctaaaagaagc tcaattcatt tctgatcaac taatggtgac    1560
173  aagtgtttga tacttgggga aagtgaacta attgcaatgg taaatcagag aaaagttgac    1620
174  caatgttgct ttctctgtag atgaacaagt gagagatcac atttaaatga tgatcacttt    1680
175  ccatttaata ctttcagcag ttttagttag atgacatgta ggatgcacct aaatctaaat    1740
176  attttatcat aaatgaagag ctggtttaga ctgtatggtc actgttggaagg aggtaaatgc    1800
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178  aaaaaaaaaa aaaaaa
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181 <211> LENGTH: 896
182 <212> TYPE: PRT
183 <213> ORGANISM: Xenopus
185 <400> SEQUENCE: 5
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189  20 25 30
190  Glu Pro Pro Gly Thr Val Ile Ala Val Leu Ser Gln His Ser Ile Phe
191  35 40 45
192  Asn Thr Thr Asp Ile Pro Ala Thr Asn Phe Arg Leu Met Lys Gln Phe
193  50 55 60
194  Asn Asn Ser Leu Ile Gly Val Arg Glu Ser Asp Gly Gln Leu Ser Ile
195  65 70 75 80
196  Met Glu Arg Ile Asp Arg Glu Gln Ile Cys Arg Gln Ser Leu His Cys
197  85 90 95
198  Asn Leu Ala Leu Asp Val Val Ser Phe Ser Lys Gly His Phe Lys Leu
199  100 105 110
200  Leu Asn Val Lys Val Glu Val Arg Asp Ile Asn Asp His Ser Pro His
201  115 120 125
202  Phe Pro Ser Glu Ile Met His Val Glu Val Ser Glu Ser Ser Ser Val
203  130 135 140
204  Gly Thr Arg Ile Pro Leu Glu Ile Ala Ile Asp Glu Asp Val Gly Ser
205  145 150 155 160
206  Asn Ser Ile Gln Asn Phe Gln Ile Ser Asn Asn Ser His Phe Ser Ile
207  165 170 175
208  Asp Val Leu Thr Arg Ala Asp Gly Val Lys Tyr Ala Asp Leu Val Leu
209  180 185 190
210  Met Arg Glu Leu Asp Arg Glu Ile Gln Pro Thr Tyr Ile Met Glu Leu

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211          195          200          205
212 Leu Ala Met Asp Gly Gly Val Pro Ser Leu Ser Gly Thr Ala Val Val
213          210          215          220
214 Asn Ile Arg Val Leu Asp Phe Asn Asp Asn Ser Pro Val Phe Glu Arg
215          225          230          235          240
216 Ser Thr Ile Ala Val Asp Leu Val Glu Asp Ala Pro Leu Gly Tyr Leu
217          245          250          255
218 Leu Leu Glu Leu His Ala Thr Asp Asp Asp Glu Gly Val Asn Gly Glu
219          260          265          270
220 Ile Val Tyr Gly Phe Ser Thr Leu Ala Ser Gln Glu Val Arg Gln Leu
221          275          280          285
222 Phe Lys Ile Asn Ser Arg Thr Gly Ser Val Thr Leu Glu Gly Gln Val
223          290          295          300
224 Asp Phe Glu Thr Lys Gln Thr Tyr Glu Phe Glu Val Gln Ala Gln Asp
225          305          310          315          320
226 Leu Gly Pro Asn Pro Leu Thr Ala Thr Cys Lys Val Thr Val His Ile
227          325          330          335
228 Leu Asp Val Asn Asp Asn Thr Pro Ala Ile Thr Ile Thr Pro Leu Thr
229          340          345          350
230 Thr Val Asn Ala Gly Val Ala Tyr Ile Pro Glu Thr Ala Thr Lys Glu
231          355          360          365
232 Asn Phe Ile Ala Leu Ile Ser Thr Thr Asp Arg Ala Ser Gly Ser Asn
233          370          375          380
234 Gly Gln Val Arg Cys Thr Leu Tyr Gly His Glu His Phe Lys Leu Gln
235          385          390          395          400
236 Gln Ala Tyr Glu Asp Ser Tyr Met Ile Val Thr Thr Ser Thr Leu Asp
237          405          410          415
238 Arg Glu Asn Ile Ala Ala Tyr Ser Leu Thr Val Val Ala Glu Asp Leu
239          420          425          430
240 Gly Phe Pro Ser Leu Lys Thr Lys Lys Tyr Tyr Thr Val Lys Val Ser
241          435          440          445
242 Asp Glu Asn Asp Asn Ala Pro Val Phe Ser Lys Pro Gln Tyr Glu Ala
243          450          455          460
244 Ser Ile Leu Glu Asn Asn Ala Pro Gly Ser Tyr Ile Thr Thr Val Ile
245          465          470          475          480
246 Ala Arg Asp Ser Asp Ser Asp Gln Asn Gly Lys Val Asn Tyr Arg Leu
247          485          490          495
248 Val Asp Ala Lys Val Met Gly Gln Ser Leu Thr Thr Phe Val Ser Leu
249          500          505          510
250 Asp Ala Asp Ser Gly Val Leu Arg Ala Val Arg Ser Leu Asp Tyr Glu
251          515          520          525
252 Lys Leu Lys Gln Leu Asp Phe Glu Ile Glu Ala Ala Asp Asn Gly Ile
253          530          535          540
254 Pro Gln Leu Ser Thr Arg Val Gln Leu Asn Leu Arg Ile Val Asp Gln
255          545          550          555          560
256 Asn Asp Asn Cys Pro Val Ile Thr Asn Pro Leu Leu Asn Asn Gly Ser
257          565          570          575
258 Gly Glu Val Leu Leu Pro Ile Ser Ala Pro Gln Asn Tyr Leu Val Phe
259          580          585          590

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VERIFICATION SUMMARY

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L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date